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Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Tue Jun 05 19:54:47 EDT 2007

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Application No: 10507446 Version No: 2.1

Input Set:

Output Set:

Started: 2007-06-05 19:54:40.016
Finished: 2007-06-05 19:54:40.692
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 676 ms
Total Warnings: 6
Total Errors: 6
No. of SeqIDs Defined: 10
Actual SeqID Count: 10

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (10)

SEQUENCE LISTING

<110> GOTO, Hidetsugu
NAKANO, Shigeru

<120> GENE PARTICIPATING IN ACETIC ACID TOLERANCE, ACETIC ACID BACTERIA
BRED USING THE GENE, AND PROCESS FOR PRODUCING VINEGAR WITH THE
USE OF THE ACETIC ACID BACTERIA

<130> 4439-4024

<140> US/10/507,446

<141> 2004-09-13

<150> PCT/JP03/02946

<151> 2003-03-12

<160> 10

<170> PatentIn version 3.2

<210> 1

<211> 2016

<212> DNA

<213> Gluconacetobacter entanii

<400> 1

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<212> PRT

<213> Gluconacetobacter entanii

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35 40 45

Phe Gly Thr Asn Asn Tyr Leu Gly Leu Ser Gln Ser Pro Ala Ala Ile
50 55 60

Glu Ala Ala Val Glu Ala Ala Arg Ala Tyr Gly Val Gly Thr Thr Gly
65 70 75 80

Ser Arg Ile Ala Asn Gly Thr Gln Gly Leu His Arg Gln Leu Glu Glu
85 90 95

Arg Leu Cys Thr Phe Phe Arg Arg Arg His Cys Met Val Phe Ser Thr
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Gly Tyr Gln Ala Asn Leu Gly Thr Ile Ser Ala Leu Ala Gly Lys Asp
115 120 125

Asp Tyr Leu Leu Leu Asp Ala Asp Ser His Ala Ser Ile Tyr Asp Gly
130 135 140

Ser Arg Leu Gly His Ala Gln Val Ile Arg Phe Arg His Asn Asp Ala
145 150 155 160

Asp Asp Leu His Lys Arg Leu Arg Arg Leu Asp Gly Thr Pro Gly Ala
165 170 175

Lys Leu Val Val Val Glu Gly Ile Tyr Ser Met Met Gly Asp Val Val
180 185 190

Pro Met Ala Glu Phe Ala Ala Val Lys Arg Glu Thr Gly Ala Trp Leu
195 200 205

Leu Ala Asp Glu Ala His Ser Val Gly Val Met Gly Glu His Gly Arg
210 215 220

Gly Val Ala Glu Ser Asp Gly Val Glu Asp Asp Val Asp Phe Val Val
225 230 235 240

Gly Thr Phe Ser Lys Ser Leu Gly Thr Val Gly Gly Tyr Cys Val Ser
245 250 255

Asn His Ala Gly Leu Asp Leu Ile Arg Leu Cys Ser Arg Pro Tyr Met
260 265 270

Phe Thr Ala Ser Leu Pro Pro Glu Val Ile Ala Ala Thr Met Ala Ala
275 280 285

Leu Thr Glu Leu Glu Asn Arg Pro Glu Leu Arg Val Arg Leu Met Asp
290 295 300

Asn Ala Arg Arg Leu His Asp Gly Leu Gln Ala Ala Gly Leu Arg Thr
305 310 315 320

Gly Pro Gln Ala Ser Pro Val Val Ser Val Ile Leu Asp Asp Val Ala
325 330 335

Val Ala Val Ala Phe Trp Asn Arg Leu Leu Asp Leu Gly Val Tyr Val
340 345 350

Asn Leu Ser Leu Pro Pro Ala Thr Pro Asp Gln His Pro Leu Leu Arg
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<213> *Acetobacter aceti*

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gctggcagggt aaggatgacc acctgtttct ggatgctgat agccacgcca gtatctatga 540
tggcagccgc ctgagtgcag cagaagttat tcgcttccgc cataatgatc cagacaacct 600

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aacaggcgct tacctgctgg tagatgaagc ccattctttt ggcgtgttgg gtcaaaatgg      780
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cgcaacccca gttattgccg ttacattgga aacagctgaa gaagctattc ccatgtggaa     1140
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Lys Pro Val Ser Ser Thr Val Gly Ile Ile Glu Gly Arg Glu Thr Leu
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Leu Phe Gly Thr Asn Asn Tyr Leu Gly Leu Ser Gln Ser Lys Asn Ala
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Ile Gln Ala Ala Gln Gln Ala Ala Ala Cys Gly Val Gly Thr Thr
65           70           75          80

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Gly Ser Arg Ile Ala Asn Gly Thr Gln Ser Leu His Arg Gln Leu Glu
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Lys Asp Ile Ala Ala Phe Phe Gly Arg Arg Asp Ala Met Val Phe Ser
100 105 110

Thr Gly Tyr Gln Ala Asn Leu Gly Ile Ile Ser Thr Leu Ala Gly Lys
115 120 125

Asp Asp His Leu Phe Leu Asp Ala Asp Ser His Ala Ser Ile Tyr Asp
130 135 140

Gly Ser Arg Leu Ser Ala Ala Glu Val Ile Arg Phe Arg His Asn Asp
145 150 155 160

Pro Asp Asn Leu Tyr Lys Arg Leu Lys Arg Met Asp Gly Thr Pro Gly
165 170 175

Ala Lys Leu Ile Val Val Glu Gly Ile Tyr Ser Met Thr Gly Asn Val
180 185 190

Ala Pro Ile Ala Glu Phe Val Ala Val Lys Lys Glu Thr Gly Ala Tyr
195 200 205

Leu Leu Val Asp Glu Ala His Ser Phe Gly Val Leu Gly Gln Asn Gly
210 215 220

Arg Gly Ala Ala Glu Ala Asp Gly Val Glu Ala Asp Val Asp Phe Val
225 230 235 240

Val Gly Thr Phe Ser Lys Ser Leu Gly Thr Val Gly Gly Tyr Cys Val
245 250 255

Ser Asp His Pro Glu Leu Glu Phe Val Arg Leu Asn Cys Arg Pro Tyr
260 265 270

Met Phe Thr Ala Ser Leu Pro Pro Glu Val Ile Ala Ala Thr Thr Ala
275 280 285

Ala Leu Lys Asp Met Gln Ala His Pro Glu Leu Arg Lys Gln Leu Met
290 295 300

Ala Asn Ala Gln Gln Leu His Ala Gly Phe Val Asp Ile Gly Leu Asn
305 310 315 320

Ala Ser Lys His Ala Thr Pro Val Ile Ala Val Thr Leu Glu Thr Ala
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Glu Glu Ala Ile Pro Met Trp Asn Arg Leu Leu Glu Leu Gly Val Tyr
340 345 350

Val Asn Leu Ser Leu Pro Pro Ala Thr Pro Asp Ser Arg Pro Leu Leu
355 360 365

Arg Cys Ser Val Met Ala Thr His Thr Pro Glu Gln Ile Ala Gln Ala
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385 390 395 400

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 <400> 10
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